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<b>(21) International Application Number:</b> PCT/US98/08336 <b>(22) International Filing Date:</b> 24 April 1998 (24.04.98)  <b>(30) Priority Data:</b> 08/845,296 25 April 1997 (25.04.97) US 09/065,125 23 April 1998 (23.04.98) US  <b>(71) Applicant:</b> GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US).  <b>(72) Inventors:</b> JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US).  <b>(74) Agent:</b> SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US).			<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
<b>(54) Title:</b> SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM			
<b>(57) Abstract</b>  Polynucleotides and the proteins encoded thereby are disclosed.			

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## SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

10        This application is a continuation-in-part of Ser. No. 60/XXX,XXX (converted to a provisional application from non-provisional application Ser. No. 08/845,296), filed April 25, 1997, which is incorporated by reference herein.

### FIELD OF THE INVENTION

15        The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

### BACKGROUND OF THE INVENTION

20        Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in  
25        the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of  
30        DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5           (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 99 to nucleotide 902;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID  
10       NO:1 from nucleotide 162 to nucleotide 902;
- (d)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 219;
- (e)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ci25\_4 deposited under accession number  
15       ATCC 98415;
- (f)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ci25\_4 deposited under accession number ATCC 98415;
- (g)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ci25\_4 deposited under accession number ATCC  
20       98415;
- (h)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ci25\_4 deposited under accession number ATCC 98415;
- (i)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- 25       (j)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:2;
- (k)     a polynucleotide which is an allelic variant of a polynucleotide of  
30       (a)-(h) above;
- (l)     a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 99 to nucleotide 902; the nucleotide sequence of SEQ ID NO:1 from nucleotide 162 to nucleotide 902; the nucleotide sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 219; the nucleotide sequence of the full-length protein coding  
5 sequence of clone ci25\_4 deposited under accession number ATCC 98415; or the nucleotide sequence of a mature protein coding sequence of clone ci25\_4 deposited under accession number ATCC 98415. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ci25\_4 deposited under accession number ATCC 98415.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:2;  
(b) fragments of the amino acid sequence of SEQ ID NO:2 comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:2; and  
(c) the amino acid sequence encoded by the cDNA insert of clone  
20 ci25\_4 deposited under accession number ATCC 98415;  
the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;  
(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 283 to nucleotide 1158;  
(c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:3 from nucleotide 1 to nucleotide 789;  
(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone da228\_6 deposited under accession number ATCC 98415;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone da228\_6 deposited under accession number ATCC 98415;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone da228\_6 deposited under accession number  
5 ATCC 98415;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone da228\_6 deposited under accession number ATCC 98415;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- 10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 141 to amino acid 150 of SEQ ID NO:4;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
15 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 283 to nucleotide 1158; the nucleotide sequence of SEQ ID NO:3 from nucleotide 1 to nucleotide 789; the nucleotide sequence of the full-length protein coding sequence of clone da228\_6 deposited under accession number ATCC 98415; or the nucleotide sequence of a mature protein coding sequence of clone da228\_6 deposited  
25 under accession number ATCC 98415. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone da228\_6 deposited under accession number ATCC 98415. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 169.
- 30 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
- (b) the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 169;
- (c) fragments of the amino acid sequence of SEQ ID NO:4 comprising the amino acid sequence from amino acid 141 to amino acid 150 of SEQ ID NO:4; and
- (d) the amino acid sequence encoded by the cDNA insert of clone da228\_6 deposited under accession number ATCC 98415;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4 or the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 169.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 152 to nucleotide 2182;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 2 to nucleotide 931;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone du410\_5 deposited under accession number ATCC 98415;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone du410\_5 deposited under accession number ATCC 98415;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone du410\_5 deposited under accession number ATCC 98415;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone du410\_5 deposited under accession number ATCC 98415;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment

comprising the amino acid sequence from amino acid 333 to amino acid 342 of SEQ ID NO:6;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

5 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 152 to nucleotide 2182; the nucleotide sequence of SEQ ID NO:5 from nucleotide 2 to nucleotide 931; the nucleotide sequence of the full-length protein coding sequence of clone du410\_5 deposited under accession number ATCC 98415; or the nucleotide sequence of a mature protein coding sequence of clone du410\_5 deposited under accession number ATCC 98415. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone du410\_5 deposited under accession number ATCC 98415. In yet other preferred  
10  
15  
embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 260.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.  
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In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;  
25 (b) the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 260;

(c) fragments of the amino acid sequence of SEQ ID NO:6 comprising the amino acid sequence from amino acid 333 to amino acid 342 of SEQ ID NO:6; and

30 (d) the amino acid sequence encoded by the cDNA insert of clone du410\_5 deposited under accession number ATCC 98415;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6 or the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 260.



In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 51 to nucleotide 611;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 1 to nucleotide 525;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone eh80\_1 deposited under accession number ATCC 98415;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone eh80\_1 deposited under accession number ATCC 98415;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
15 protein coding sequence of clone eh80\_1 deposited under accession number ATCC 98415;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone eh80\_1 deposited under accession number ATCC 98415;
- (h) a polynucleotide encoding a protein comprising the amino acid  
20 sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 88 to amino acid 97 of SEQ ID NO:8;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 51 to nucleotide 611; the nucleotide sequence of SEQ ID NO:7 from nucleotide 1 to nucleotide 525; the nucleotide sequence of the full-length protein coding sequence of clone eh80\_1 deposited under accession number ATCC 98415; or the

nucleotide sequence of a mature protein coding sequence of clone eh80\_1 deposited under accession number ATCC 98415. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone eh80\_1 deposited under accession number ATCC 98415. In yet other preferred embodiments,  
5 the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8 from amino acid 1 to amino acid 158.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

In other embodiments, the present invention provides a composition comprising  
10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- (b) the amino acid sequence of SEQ ID NO:8 from amino acid 1 to amino acid 158;
- 15 (c) fragments of the amino acid sequence of SEQ ID NO:8 comprising the amino acid sequence from amino acid 88 to amino acid 97 of SEQ ID NO:8; and
- (d) the amino acid sequence encoded by the cDNA insert of clone eh80\_1 deposited under accession number ATCC 98415;

the protein being substantially free from other mammalian proteins. Preferably such  
20 protein comprises the amino acid sequence of SEQ ID NO:8 or the amino acid sequence of SEQ ID NO:8 from amino acid 1 to amino acid 158.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 431 to nucleotide 559;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 518 to nucleotide 559;
- 30 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 190 to nucleotide 547;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone er369\_1 deposited under accession number ATCC 98415;

- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone er369\_1 deposited under accession number ATCC 98415;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone er369\_1 deposited under accession number ATCC 98415;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone er369\_1 deposited under accession number ATCC 98415;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 16 to amino acid 25 of SEQ ID NO:10;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j).
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 431 to nucleotide 559; the nucleotide sequence of SEQ ID NO:9 from nucleotide 518 to nucleotide 559; the nucleotide sequence of SEQ ID NO:9 from nucleotide 190 to nucleotide 547; the nucleotide sequence of the full-length protein coding sequence of clone er369\_1 deposited under accession number ATCC 98415; or the nucleotide sequence of a mature protein coding sequence of clone er369\_1 deposited under accession number ATCC 98415. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone er369\_1 deposited under accession number ATCC 98415. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10 from amino acid 1 to amino acid 39.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
  - 5 (b) the amino acid sequence of SEQ ID NO:10 from amino acid 1 to amino acid 39;
  - (c) fragments of the amino acid sequence of SEQ ID NO:10 comprising the amino acid sequence from amino acid 16 to amino acid 25 of SEQ ID NO:10; and
  - 10 (d) the amino acid sequence encoded by the cDNA insert of clone er369\_1 deposited under accession number ATCC 98415;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10 or the amino acid sequence of SEQ ID NO:10 from amino acid 1 to amino acid 39.

15 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:11 from nucleotide 91 to nucleotide 2838;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 2209 to nucleotide 2838;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 839 to nucleotide 1197;
- 25 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fh123\_5 deposited under accession number ATCC 98415;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fh123\_5 deposited under accession number ATCC 98415;
- 30 (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fh123\_5 deposited under accession number ATCC 98415;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fh123\_5 deposited under accession number ATCC 98415;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 453 to amino acid 462 of SEQ ID NO:12;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 91 to nucleotide 2838; the nucleotide sequence of SEQ ID NO:11 from nucleotide 2209 to nucleotide 2838; the nucleotide sequence of SEQ ID NO:11 from nucleotide 839 to nucleotide 1197; the nucleotide sequence of the full-length protein coding sequence of clone fh123\_5 deposited under accession number ATCC 98415; or the nucleotide sequence of a mature protein coding sequence of clone fh123\_5 deposited under accession number ATCC 98415. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fh123\_5 deposited under accession number ATCC 98415. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12 from amino acid 251 to amino acid 369.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:12;

(b) the amino acid sequence of SEQ ID NO:12 from amino acid 251 to amino acid 369;

(c) fragments of the amino acid sequence of SEQ ID NO:12 comprising the amino acid sequence from amino acid 453 to amino acid 462 of SEQ ID NO:12; and

5 (d) the amino acid sequence encoded by the cDNA insert of clone fh123\_5 deposited under accession number ATCC 98415; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12 or the amino acid sequence of SEQ ID NO:12 from amino acid 251 to amino acid 369.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 568 to nucleotide 978;

15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 1084 to nucleotide 1854;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fm60\_1 deposited under accession number ATCC 98415;

20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fm60\_1 deposited under accession number ATCC 98415;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fm60\_1 deposited under accession number ATCC 98415;

25 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fm60\_1 deposited under accession number ATCC 98415;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

30 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:14;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 568 to nucleotide 978; the nucleotide sequence of SEQ ID NO:13 from nucleotide 1084 to nucleotide 1854; the nucleotide sequence of the full-length protein coding sequence of clone fm60\_1 deposited under accession number ATCC 98415; or the nucleotide sequence of a mature protein coding sequence of clone fm60\_1 deposited under  
10 accession number ATCC 98415. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fm60\_1 deposited under accession number ATCC 98415.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:14;

(b) fragments of the amino acid sequence of SEQ ID NO:14 comprising  
20 the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:14; and

(c) the amino acid sequence encoded by the cDNA insert of clone fm60\_1 deposited under accession number ATCC 98415; the protein being substantially free from other mammalian proteins. Preferably such  
25 protein comprises the amino acid sequence of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 16 to nucleotide 309;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 127 to nucleotide 309;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fr473\_2 deposited under accession number ATCC 98415;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fr473\_2 deposited under accession number ATCC 98415;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fr473\_2 deposited under accession number ATCC 98415;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fr473\_2 deposited under accession number ATCC 98415;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:16;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 16 to nucleotide 309; the nucleotide sequence of SEQ ID NO:15 from nucleotide 127 to nucleotide 309; the nucleotide sequence of the full-length protein coding sequence of clone fr473\_2 deposited under accession number ATCC 98415; or the nucleotide sequence of a mature protein coding sequence of clone fr473\_2 deposited under accession number ATCC 98415. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fr473\_2 deposited under accession number ATCC 98415. In yet other preferred  
30 embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 58.



Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
- (b) the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 58;
- (c) fragments of the amino acid sequence of SEQ ID NO:16 comprising  
10 the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:16;  
and
- (d) the amino acid sequence encoded by the cDNA insert of clone fr473\_2 deposited under accession number ATCC 98415;

the protein being substantially free from other mammalian proteins. Preferably such  
15 protein comprises the amino acid sequence of SEQ ID NO:16 or the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 58.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions.  
20 Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such  
25 polynucleotide compositions in a suitable culture medium; and
- (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

30 Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically

effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

#### BRIEF DESCRIPTION OF THE DRAWINGS

5        Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

#### DETAILED DESCRIPTION

##### ISOLATED PROTEINS AND POLYNUCLEOTIDES

10        Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino  
15        acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

20        As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins  
25        which are transported across the membrane of the endoplasmic reticulum.

##### Clone "ci25\_4"

A polynucleotide of the present invention has been identified as clone "ci25\_4". ci25\_4 was isolated from a human adult brain cDNA library using methods which are  
30        selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ci25\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ci25\_4 protein").

The nucleotide sequence of ci25\_4 as presently determined is reported in SEQ ID NO:1. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ci25\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 9 to 21 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22, or are a transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ci25\_4 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for ci25\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ci25\_4 demonstrated at least some similarity with sequences identified as AA243050 (zr24h03.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664373 5'), AA316800 (EST188485 HCC cell line (matatasis to liver in mouse) II Homo sapiens cDNA 5' end), AA340783 (EST46083 Fetal kidney II Homo sapiens cDNA 5' end), Q05686 (Islets of Langerhans cell clone ICA12.3 (ATCC 40703)), R12690 (yf40e07.s1 Homo sapiens cDNA clone 129348 3'), R16432 (yf40e07.r1 Homo sapiens cDNA clone), W81653 (zd84d12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347351 5'), and W81654 (zd84d12.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347351 3'). Based upon sequence similarity, ci25\_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the ci25\_4 protein sequence, centered around amino acids 81, 134, 159, 182, and 241 of SEQ ID NO:2, respectively.

#### 25        Clone "da228\_6"

A polynucleotide of the present invention has been identified as clone "da228\_6". da228\_6 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. da228\_6 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "da228\_6 protein").

The nucleotide sequence of da228\_6 as presently determined is reported in SEQ ID NO:3. What applicants presently believe to be the proper reading frame and the

predicted amino acid sequence of the da228\_6 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone da228\_6 should be approximately 1500 bp.

- 5 The nucleotide sequence disclosed herein for da228\_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. da228\_6 demonstrated at least some similarity with sequences identified as W57906 (zd17f11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 340941 5') and W57907 (zd17f11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA  
10 clone 340941 3'. Based upon sequence similarity, da228\_6 proteins and each similar protein or peptide may share at least some activity.

Clone "du410\_5"

- A polynucleotide of the present invention has been identified as clone "du410\_5".  
15 du410\_5 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. du410\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as  
20 "du410\_5 protein").

The nucleotide sequence of du410\_5 as presently determined is reported in SEQ ID NO:5. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the du410\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6.

- 25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone du410\_5 should be approximately 2400 bp.

- The nucleotide sequence disclosed herein for du410\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. du410\_5 demonstrated at least some similarity with sequences  
30 identified as N44315 (EST51p19 WATM1 Homo sapiens cDNA clone 51p19) and N66980 (yz58d04.s1 Homo sapiens cDNA clone 287239 3'). The predicted amino acid sequence disclosed herein for du410\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted du410\_5 protein demonstrated at least some similarity to sequences identified as U67604 (P115 protein

[*Methanococcus jannaschii*]). Based upon sequence similarity, du410\_5 proteins and each similar protein or peptide may share at least some activity.

Clone "eh80\_1"

5 A polynucleotide of the present invention has been identified as clone "eh80\_1". eh80\_1 was isolated from a human adult blood (peripheral blood mononuclear cells treated with granulocyte-colony stimulating factor *in vivo*) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
10 analysis of the amino acid sequence of the encoded protein. eh80\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "eh80\_1 protein").

The nucleotide sequence of eh80\_1 as presently determined is reported in SEQ ID NO:7. What applicants presently believe to be the proper reading frame and the predicted  
15 amino acid sequence of the eh80\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8. Another potential eh80\_1 reading frame and predicted amino acid sequence is encoded by basepairs 41 to 1659 of SEQ ID NO:7 and is reported in SEQ ID NO:25. A frameshift in the nucleotide sequence of SEQ ID NO:5 between about nucleotide 41 to about nucleotide 614 could join together portions of the  
20 overlapping reading frames of SEQ ID NO:8 and SEQ ID NO:25.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone eh80\_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for eh80\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
25 FASTA search protocols. eh80\_1 demonstrated at least some similarity with sequences identified as AA012957 (ze27b03.r1 Soares retina N2b4HR Homo sapiens cDNA clone 360173 5'), AA019878 (ze63b03.s1 Soares retina N2b4HR Homo sapiens cDNA clone 363629 3'), AA505456 (nh84c07.s1 NCI\_CGAP\_Br1.1 Homo sapiens cDNA clone IMAGE 965196), Q60246 (Human brain Expressed Sequence Tag EST02242), R16603 (yf43c04.r1  
30 Homo sapiens cDNA clone 129606 5'), and T85469 (yd82f05.r1 Homo sapiens cDNA clone 114753 5'). The predicted amino acid sequence disclosed herein for eh80\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted eh80\_1 protein demonstrated at least some similarity to sequences identified as U40747 (FBP 11 [*Mus musculus*])). Based upon sequence

similarity, eh80\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the amino acid sequence of SEQ ID NO:8, one centered around amino acid 107 and another around amino acid 131.

5

Clone "er369\_1"

A polynucleotide of the present invention has been identified as clone "er369\_1". er369\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
10 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. er369\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "er369\_1 protein").

The nucleotide sequence of er369\_1 as presently determined is reported in SEQ ID  
15 NO:9. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the er369\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 17 to 29 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30, or are a transmembrane domain.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone er369\_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for er369\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. er369\_1 demonstrated at least some similarity with sequences  
25 identified as H12227 (ym12g10.r1 Homo sapiens cDNA clone 47729 5'), H70978 (yr73g06.r1 Homo sapiens cDNA clone 210970 5'), M79179 (EST01327 Homo sapiens cDNA clone HHCPO81), Q61324 (Human brain Expressed Sequence Tag EST01327), and R53554 (yg84e04.s1 Homo sapiens cDNA clone 39854 3' similar to contains Alu repetitive element). Based upon sequence similarity, er369\_1 proteins and each similar protein or  
30 peptide may share at least some activity. The nucleotide sequence of er369\_1 indicates that it may contain an Alu repetitive element.

Clone "fh123\_5"

A polynucleotide of the present invention has been identified as clone "fh123\_5". fh123\_5 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fh123\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fh123\_5 protein").

The nucleotide sequence of fh123\_5 as presently determined is reported in SEQ ID  
10 NO:11. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fh123\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino acids 694 to 706 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 707, or are a transmembrane domain.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fh123\_5 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for fh123\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fh123\_5 demonstrated at least some similarity with sequences  
20 identified as AA815253 (ai64d02.s1 Soares testis NHT Homo sapiens cDNA clone 1375587 3'), AA855689 (vw71h04.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone 1260439 5'), and W80785 (zd83d07.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347245 3). The predicted amino acid sequence disclosed herein for fh123\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the  
25 BLASTX search protocol. The predicted fh123\_5 protein demonstrated at least some similarity to sequences identified as D80005 (KIAA0183 [Homo sapiens]). Based upon sequence similarity, fh123\_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional possible transmembrane domains within the fh123\_5 protein sequence.

30

Clone "fm60\_1"

A polynucleotide of the present invention has been identified as clone "fm60\_1". fm60\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was

identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fm60\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fm60\_1 protein").

5       The nucleotide sequence of fm60\_1 as presently determined is reported in SEQ ID NO:13. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fm60\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14.

10       The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fm60\_1 should be approximately 2200 bp.

15       The nucleotide sequence disclosed herein for fm60\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fm60\_1 demonstrated at least some similarity with sequences identified as AA155574 (zo70a01.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592200 3'), AF015147 (Homo sapiens clone HS19.1 Alu-Ya5 sequence), N86095 (J6377F Fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J6377 5' similar to REPETITIVE ELEMENT ALU), U14567 (\*\*ALU WARNING Human Alu-J subfamily consensus sequence), and Z82199 (Human DNA sequence from clone J316D5). Based upon sequence similarity, fm60\_1 proteins and each similar protein or peptide may share  
20       at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the fm60\_1 protein sequence centered around amino acid 50 of SEQ ID NO:14. The nucleotide sequence of fm60\_1 indicates that it may contain one or more of the following repetitive elements: Alu, L1.

25       Clone "fr473\_2"

30       A polynucleotide of the present invention has been identified as clone "fr473\_2". fr473\_2 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fr473\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fr473\_2 protein").

      The nucleotide sequence of fr473\_2 as presently determined is reported in SEQ ID NO:15. What applicants presently believe to be the proper reading frame and the



predicted amino acid sequence of the fr473\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16. Amino acids 25 to 37 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 38, or are a transmembrane domain. Amino acids 62 to 74 are another possible  
5 leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 75, or are a transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fr473\_2 should be approximately 605 bp.

The nucleotide sequence disclosed herein for fr473\_2 was searched against the  
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fr473\_2 demonstrated at least some similarity with sequences identified as AA479559 (zu42a02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740618 5' similar to WP:F49C12.12 CE03372), H46855 (yo18g04.r1 Homo sapiens cDNA clone 178326 5'), T24372 (Human gene signature HUMGS06404), W31692  
15 (zb93d01.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320353 5'), and Z32877 (H. sapiens partial cDNA sequence; clone HEA41P; single read). The predicted amino acid sequence disclosed herein for fr473\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fr473\_2 protein demonstrated at least some similarity to sequences identified  
20 as Z68227 (F49C12.12 [Caenorhabditis elegans]). Based upon sequence similarity, fr473\_2 proteins and each similar protein or peptide may share at least some activity.

#### Deposit of Clones

Clones ci25\_4, da228\_6, du410\_5, eh80\_1, er369\_1, fh123\_5, fm60\_1, and fr473\_2  
25 were deposited on April 25, 1997 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98415, from which each clone comprising a particular polynucleotide is obtainable. All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the  
30 granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in this composite deposit. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the

appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

<u>Clone</u>	<u>Probe Sequence</u>
ci25_4	SEQ ID NO:17
da228_6	SEQ ID NO:18
25 du410_5	SEQ ID NO:19
eh80_1	SEQ ID NO:20
er369_1	SEQ ID NO:21
fh123_5	SEQ ID NO:22
fm60_1	SEQ ID NO:23
30 fr473_2	SEQ ID NO:24

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as , for example, that produced by use of biotin phosphoramidite (1-

dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

- 5           (a)    It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- (b)    It should be designed to have a  $T_m$  of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with  $\gamma$ -<sup>32</sup>P ATP (specific activity 6000  
10   Ci/mmol) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting  
15   probe should be approximately 4e+6 dpm/pmol.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 µl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 µg/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in  
20   fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 µg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

25           Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 µg/ml of yeast RNA, and 10 mM EDTA (approximately  
30   10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes.

A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

- 5           The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

          Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the  
10   protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, *Bio/Technology* 10, 773-778 (1992) and in R.S. McDowell, *et al.*, *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding  
15   sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

- 20           The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or  
25   other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

          The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are  
30   derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed

herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates*

*conicolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created

5 allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs,

10 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least

15 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and

20 screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly

25 stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>‡</sup>	Hybridization Temperature and Buffer <sup>†</sup>	Wash Temperature and Buffer <sup>†</sup>
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	<50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	<50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	RNA:RNA	<50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
10	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	<50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	<50	T <sub>J</sub> *; 4xSSC	T <sub>J</sub> *; 4xSSC
	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	<50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
15	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	<50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	DNA:RNA	<50	T <sub>P</sub> *; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	<50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

<sup>‡</sup>: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

<sup>†</sup>: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).



Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds.,

5 John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or  
10 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide of the invention may be operably linked to an  
15 expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably  
20 linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the  
25 protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

30 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial

strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant

methyle or other aliphatic groups; can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance  
5 with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

10 The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith,  
15 including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally  
20 provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another  
25 amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be  
30 expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

## USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

### Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine

levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially  
5 binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

10 Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook,  
15 J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as  
20 nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or  
25 capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either  
30 inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is

evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

- 5           The activity of a protein of the invention may, among other means, be measured by the following methods:

          Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-  
10   Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

- 15           Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in*  
20   *Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons,  
25   Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human  
30   Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for

example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or



tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of

viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient  
5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic  
10 acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function  
15 (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides.  
20 For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used  
25 to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II  
30 molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface.

Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

10           The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnoli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

25           Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

30           Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter

7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent

myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of  
5 hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or  
10 *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et  
20 al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of*  
25 *Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359,  
30 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

#### Tissue Growth Activity

5 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

10 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of  
15 congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce  
20 differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

25 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and  
30 other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of

congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce  
5 differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in  
10 the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve  
15 tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present  
20 invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of  
25 non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac)  
30 and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting  
5 differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described  
10 in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

Assays for wound healing activity include, without limitation, those described in:  
Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year  
15 Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related  
20 activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals  
25 and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example,  
30 United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:



Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

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#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells.

- 10 Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses
- 15 against the tumor or infecting agent.

- A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population
- 20 of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- Assays for chemotactic activity (which will identify proteins that induce or prevent
- 25 chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene
- 30 Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al. *APMIS* 103:140-146, 1995; Muller et al. *Eur. J. Immunol.* 25: 1744-1748; Gruber et al. *J. of Immunol.* 152:5860-5867, 1994; Johnston et al. *J. of Immunol.* 153: 1762-1768, 1994.

### Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

10 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 15 35:467-474, 1988.

### Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and

Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 5 1995.

#### Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in 10 the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat 15 inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting 20 from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

#### Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major 25 roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

30 The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the

first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

5           E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and  
10 their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention  
15 encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue  
20 in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and  
25 polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the  
30 cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used

to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides  
5 encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

#### 10 Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or  
15 tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### 20 Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height,  
25 weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein,  
30 carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic

lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen

5 in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### ADMINISTRATION AND DOSING

10 A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term

15 "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11,

20 IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention,

25 or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

30 A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be

administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be  
5 administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic  
10 factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection.  
15 Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or  
20 an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain  
25 physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

30 When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred



pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The  
5 pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone.  
10 Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not  
15 increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1mg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous  
20 therapy using the pharmaceutical composition of the present invention.  
25

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the  
30 carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, *J. Amer.Chem.Soc.* 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, *FEBS Lett.* 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal

antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting  
5 and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When  
10 administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also  
15 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the  
20 developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular  
25 application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins  
30 or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-

aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns.

- 5 In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, 10 ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 15 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

20 In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

25 The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering 30 various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in

the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline  
5 labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without  
10 limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

15 Patent and literature references cited herein are incorporated by reference as if fully set forth.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth  
McCoy, John M.  
LaVallie, Edward R.  
Racie, Lisa A.  
Merberg, David  
Treacy, Maurice  
Spaulding, Vikki  
Agostino, Michael J.
- (ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Genetics Institute, Inc.
  - (B) STREET: 87 CambridgePark Drive
  - (C) CITY: Cambridge
  - (D) STATE: MA
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
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## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1480 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

AGGCGCCCTC CCTTCCTGAG GAGCTGTTGG CCTGGGTGGG CAGGAACTGC AGTATGGCCA      60
TGGGCTGAGC AGGCTGAGCA CCTCAGCCTT TAGGGCTTAT GGCCAGGGGA CACTGTATGA      120
CTCTCCTCTC CTGCAGGTGT CTATCCACCT GGGGTATGGC ATCTACCGAC CTGTCTCCCT      180
GGGGTCACAT GCTTTGTTC CATTCCTGTC CTGGCTGGAC CAGCCACTGT GGGACCAACA      240
CCCCCCCCAC ACTCCCCCAG ACTGCTCGTC TATCACCAGG ATCGCTTTGT ACTTTGTGCA      300
AAAGGGTCTG GCTGTCCCTT GCTGTTTCA TCTCTGCCAA GCCTATTGTG CCTCTGGCTG      360
CTGTATGTGT GCGCGTGAC GTGTGTGTGT TTCATCTGTT CATTCACTGC ACAAGATATT      420
TATTGAGTGC CCACTACGTG CCAGGCACTG TTGCTGAGTT CCTGTGGGTG TGTCTCTCGA      480
TGCCACTCCT GCTTCTCTGG GGGCCTCTTT CTGTGCTTCT CTTGTCCCC AAATTGCTAC      540
CTCTTTGTCA GTCTGGGTGT CTCAGGTTCT GTGTGCTCCT GTGTGCATTT CTGTCTCTCT      600
CTGTCTCTGT CTCTCTGCAA GGCCCTCTAT TTCTCTCTTT CTGGGTGTCT GTCCTTTGCC      660
CCCTGTGCCC TCTGGATTCT CTGGGTCTAT GTAGGCCCTT GGTCTGCCCT GGGCTCATCA      720
GCCTTCCTGA CCTCCTCCTG CCCTCCCCCT CACTCCCTCC CTGGCTCTGC CAGTCGGTTC      780
CCACGGAGCC ATTTT TAGCT CTGATCAGCA TGGGAATGTG CCTCGGCCTC CAAGGGGCTT      840
TGTCTGGTG CCCCCGCCCC TGGTCCCAAC CTGATCCCAC GAGGGAGTTG GGACAGGAGG      900
ATTGATGGTG CTCCCCTTCC TGCCAGCGTC AGAGGCCCTG GAGAGGGGCT GTCCATGGCA      960
GCTGGTCTTT ATTCCTCCCT CATGAGCACA GGGTCGGGGG GTCCCCATTC TTGGAAGAGG     1020
TTGAGAAGAC TCCTGGGCTT CAGCCTCTCC CACCCAGCCC TGCCCTCAC CTGCCTGCCC     1080
TCCCCTCCCC CACTCTATAC TAGGGACTGG ATCTCAGCCT CTGATCAGTT TCACAAAGTT     1140
TGTTCCCTAA GGAAATCAAA TCCCATGTG ACCTAACTCT GAAGATCTAA ATAGCCCTTG     1200
GATCAGTACG GGAACCCCAA ATCCCACAGG GCCAGATGTG GAGTCTGTGT CTGCCCCCGT     1260
CTTCTCTCCA TCCTCAAAGC CCCCACTTCT CTCCAGGCTG TTTCTTTTTT TATGACTGTA     1320
AACATAGATA GTGCTTTATT TTGTTAATAA TAAGATAATG ATGAGTAACT TAACCAGCAC     1380
ATTTCTCCTG TTTACACTCG GGGGATTTTT TTGTTTTCTG ATGACATAAT AAAGACAGAT     1440

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CATTTTCAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

1480

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Ala Arg Gly His Cys Met Thr Leu Leu Ser Cys Arg Cys Leu Ser
1           5           10           15

Thr Trp Gly Met Ala Ser Thr Asp Leu Ser Pro Trp Gly His Met Leu
20           25           30

Cys Phe His Ser Cys Pro Gly Trp Thr Ser His Cys Gly Thr Asn Thr
35           40           45

Pro Pro Thr Leu Pro Gln Thr Ala Arg Leu Ser Pro Gly Ser Leu Cys
50           55           60

Thr Leu Cys Lys Arg Val Trp Leu Ser Leu Ala Val Phe Ile Ser Ala
65           70           75           80

Lys Pro Ile Val Pro Leu Ala Ala Val Cys Val Arg Val His Val Cys
85           90           95

Val Phe His Leu Phe Ile His Cys Thr Arg Tyr Leu Leu Ser Ala His
100          105          110

Tyr Val Pro Gly Thr Val Ala Glu Phe Leu Trp Val Cys Leu Ser Met
115          120          125

Pro Leu Leu Leu Leu Trp Gly Pro Leu Ser Val Leu Leu Phe Val Pro
130          135          140

Lys Leu Leu Pro Leu Cys Gln Ser Gly Cys Leu Arg Phe Cys Val Ser
145          150          155          160

Leu Cys Ala Phe Leu Ser Leu Ser Val Leu Val Ser Leu Gln Gly Pro
165          170          175

Leu Phe Leu Ser Phe Leu Val Ser Val Leu Cys Pro Leu Cys Pro Leu
180          185          190

Asp Ser Leu Gly Leu Cys Arg Pro Leu Val Cys Pro Gly Leu Ile Ser
195          200          205

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Leu Pro Asp Leu Leu Leu Pro Ser Pro Ser Leu Pro Pro Trp Leu Cys  
 210 215 220  
 Gln Ser Val Pro Thr Glu Pro Phe Leu Ala Leu Ile Ser Met Gly Met  
 225 230 235 240  
 Cys Leu Gly Leu Gln Gly Ala Leu Ser Trp Cys Pro Arg Pro Trp Ser  
 245 250 255  
 Gln Pro Asp Pro Thr Arg Glu Leu Gly Gln Glu Asp  
 260 265

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCGGCGGCT CCTGGAACCC CGGTTGCGGG CGATGCCAGC CACCCCAGCG AAGCCGCCGC 60  
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 TTCGCTTGCC ATCACAGCAC GCCTATCGGA TGTGAGAGGA GAAGTCCCGC TGCTCGGGCA 180  
 CTGTCTATAT ACGCCTAACA CCTACATATA TTTTAAAAAC ATTAAATATA ATTAACAATC 240  
 AAAAGAAAGA GGAGAAAGGA AGGGAAGCAT TACTGGGTTA CTATGCACTT GCGACTGATT 300  
 TCTTGGCTTT TTATCATTTT GAACTTTATG GAATACATCG GCAGCCAAAA CGCCTCCCGG 360  
 GGAAGGCGCC AGCGAAGAAT GCATCCTAAC GTTAGTCAAG GCTGCCAAGG AGGCTGTGCA 420  
 ACATGCTCAG ATTACAATGG ATGTTTGTC TGTAAAGCCA GACTATTTTT TGCTCTGGAA 480  
 AGAATTGGCA TGAAGCAGAT TGGAGTATGT CTCTCTTCAT GTCCAAGTGG ATATTATGGA 540  
 ACTCGATATC CAGATATAAA TAAGTGTAACA AAATGCAAAG CTGACTGTGA TACCTGTTTC 600  
 AACAAAAATT TCTGCACAAA ATGTAAAAGT GGATTTTACT TACACCTTGG AAAGTGCCTT 660  
 GACAATTGCC CAGAAGGGTT GGAAGCCAAC AACCATACTA TGGAGTGTGT CAGTATTGTG 720  
 CACTGTGAGG TCAGTGAATG GAATCCTTGG AGTCCATGCA CGAAGAAGGG AAAACATGT 780  
 GGCTTCAAAA GAGGGACTGA AACACGGGTC CGAGAAATAA TACAGCATCC TTCAGCAAAG 840



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GGTAACCTGT GTCCCCAAC AAATGAGACA AGAAAGTGTA CAGTGCAAAG GAAGAAGTGT      900
CAGAAGGGAG AACGAGGAAA AAAAGGAAGG GAGAGGAAAA GAAAAAAACC TAATAAAGGA      960
GAAAGTAAAG AAGCAATACC TGACAGCAAA AGTCTGGAAT CCAGCAAAGA AATCCCAGAG     1020
CAACGAGAAA ACAAACAGCA GCAGAAGAAG CGAAAAGTCC AAGATAAACA GAAATCGGGG     1080
ATTGAAGTCA CCCTAGCTGA AGGCCTCACC AGTGTTTCAC AGAGGACACA GCCCACCCTT     1140
TGCAGGAGGA GGTATCTCTG AGTGTGCAGC ACAGAATCGC ATGACCCACC TTAACCTTCC     1200
TGTTGTCATG GAAGGATGCA CGGCTGCTCT GTCCACTGTG ATTCCTAGCC CTCTCAAGAT     1260
CACTGCTTTC TGAAGAATTT GCAATGACTC TGGCTTCTGG CTGCTTATCT CTGGACACCC     1320
GTTCTCCACC AGTTGTACAG TTCATGTAAT CTAATTGGCT TAATTGATTT TCCACTTCTC     1380
TCTTCCTCTT CTAAGATATA AACATTTTAA ATGATTTAAA AAAAAAAAAA AAAAAA      1436

```

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 292 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1           5           10           15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
          20           25           30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
          35           40           45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
          50           55           60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65           70           75           80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
          85           90           95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
          100          105          110

```

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn  
 115 120 125  
 Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser  
 130 135 140  
 Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr  
 145 150 155 160  
 Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val  
 165 170 175  
 Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro  
 180 185 190  
 Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys  
 195 200 205  
 Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn  
 210 215 220  
 Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser  
 225 230 235 240  
 Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys  
 245 250 255  
 Arg Lys Val Gln Asp Lys Gln Lys Ser Gly Ile Glu Val Thr Leu Ala  
 260 265 270  
 Glu Gly Leu Thr Ser Val Ser Gln Arg Thr Gln Pro Thr Pro Cys Arg  
 275 280 285  
 Arg Arg Tyr Leu  
 290

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2322 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGTAAAGAGC AGATTAGAAC AGAAATCAGG AGAACTTGGG AAGAAGATCA CTGAGTTAAC 60  
 ATTGAAAAAT CAGACACTAC AAAAGGAAAT TGAAAAAGTT TATTTGGATA ATAAGCTCCT 120

CAAGGAGCAA GCACATAACT TAACAATTGA AATGAAAAAT CATTATGTTT CTTTAAAAGT	180
AAGTGAAGAC ATGAAAAAGT CACATGATGC AATTATTGAT GATCTTAATA GAAAGCTTTT	240
AGATGTAACA CAAAAATATA CAGAAAAGAA GTTGGAAATG GAGAAATTGC TACTGGAAAA	300
TGACAGCTTA AGTAAGGATG TAAGCCGCCT AGAAACTGTG TTTGTACCTC CTGAGAAACA	360
TGAAAAAGAG ATAATAGCTC TGAAATCCAA TATTGTTGAA CTTAAGAAAC AGCTGTCTGA	420
ACTTAAGAAA AAATGTGGTG AAGACCAGGA GAAAATACAC GCTCTCACAT CTGAAAACAC	480
TAAGTGAAG AAGATGATGA GTAATCAGTA TGTGCCAGTT AAAACCCATG AAGAGGTTAA	540
AATGACACTG AATGACACGT TAGCCAAAAC TAACAGAGAA TTATTAGATG TGAAGAAAAA	600
ATTTGAAGAT ATAAATCAGG AATTTGTAAA AATAAAAGAT AAGAATGAAA TATTAAAAAG	660
AAACCTGGAA AACACTCAGA ACCAAATAAA AGCTGAGTAC ATCAGCCTGG CAGAGCACGA	720
GGCAAAGATG AGCTCGCTAA GTCAGAGCAT GAGAAAGGTG CAGGATAGTA ATGCTGAAAT	780
CTTGGCCAAC TACAGAAAAG GCCAAGAAGA GATTGTGACA CTGCATGCCG AAATTAAAGC	840
CCAGAAGAAG GAGCTCGACA CAATACAAGA ATGCATTAAG GTAAAATATG CCCCATTGT	900
CAGCTTTGAG GAGTGCGAGA GAAAATTTAA AGCAACAGAG AAAGAACTAA AAGACCAGTT	960
ATCAGAGCAG ACACAAAAGT ATAGTGTCAG TGAAGAAGAA GTCAAGAAAA ACAAGCAAGA	1020
GAATGACAAG TTAAAGAAGG AGATTTTAC CCTTCAGAAA GATTGAGAG ATAAGACAGT	1080
TCTCATTGAG AAGTCTCATG AAATGGAAAG AGCATTAAAG AGAAAAACAG ACGAGCTAAA	1140
CAAACAGTTA AAAGACTTGT CACAGAAATA CACGGAAGTA AAGAATGTGA AAGAGAAGCT	1200
AGTAGAAGAA AATGCCAAAC AGACTTCTGA GATACTTGCA GTGCAAAATC TTTTGCAAAA	1260
ACAACATGTT CCATTGGAAC AGGTTGAGGC TCTGAAAAAA TCTCTTAATG GCACAATTGA	1320
AAATCTAAAG GAAGAACTGA AGAGTATGCA AAGGTGTTAC GAGAAAGAGC AGCAGACAGT	1380
GACCAAACTG CATCAATTGT TGGAGAATCA AAAGAACTCT TCTGTACCCC TGGCAGAGCA	1440
TTTGCAGATT AAAGAAGCAT TTGAGAAAGA AGTTGGAATC ATAAAAGCCA GCTTGAGAGA	1500
AAAGGAAGAA GAAAGCCAAA ACAAATGGA AGAAGTCTCC AAACCTCAGT CGGAGGTTCA	1560
GAATACTAAA CAAGCATTA AAAAAATTAGA GACTAGAGAG GTAGTTGACT TGTCTAAATA	1620
TAAAGCAACA AAAAGTGATT TGGAGACACA GATTCTAGC TTAAATGAAA AATTGGCCAA	1680
TCTGAATAGA AAGTATGAGG AAGTATGTGA GGAAGTTTGT CATGCCAAAA AGAAGGAAAT	1740
ATCTGCAAAA GATGAGAAGG AATTACTGCA TTTCAGCATT GAGCAAGAAA TTAAGGATCA	1800

GAAGGAACGA TGTGATAAGT CCTTAACAAC AATCACAGAG TTACAAAGAA GAATACAAGA 1860  
 ATCTGCTAAA CAAATAGAAG CAAAAGATAA TAAGATAACT GAACTGCTTA ATGATGTGGA 1920  
 AAGATTAAAA CAGGCACTCA ATGGCCTTTC CCAACTCACC TACACAAGTG GGAACCCAC 1980  
 CAAGAGGCAG AGCCAGCTGA TTGACACTCT GCAGCACCAA GTGAAATCTC TGGAGCAACA 2040  
 GCTGGCCGAT GCTGACAGAC AGCACCAAGA AGTAATTGCA ATTTATCGGA CACACCTTCT 2100  
 TAGTGCTGCA CAGGGTCACA TGGATGAAGA TGTTCAGGAG GCTCTGCTCC AGATCATACA 2160  
 AATGCGGCAG GGGCTTGTGT GCTAGCCGTT AGCACTGACT GCCAGTATCT GTTTTATCTT 2220  
 GCTGGTGCTG AACATTCTTT GTGCAACTCC ATGGTCTTTC TGGGCCTTAC TGTGCTGGTA 2280  
 TAATTAAAAT AAAATATATT TTGTTCTAAA AAAAAAAAAA AA 2322

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Lys Asn His Tyr Val Pro Leu Lys Val Ser Glu Asp Met Lys Lys  
 1 5 10 15  
 Ser His Asp Ala Ile Ile Asp Asp Leu Asn Arg Lys Leu Leu Asp Val  
 20 25 30  
 Thr Gln Lys Tyr Thr Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Leu  
 35 40 45  
 Glu Asn Asp Ser Leu Ser Lys Asp Val Ser Arg Leu Glu Thr Val Phe  
 50 55 60  
 Val Pro Pro Glu Lys His Glu Lys Glu Ile Ile Ala Leu Lys Ser Asn  
 65 70 75 80  
 Ile Val Glu Leu Lys Lys Gln Leu Ser Glu Leu Lys Lys Lys Cys Gly  
 85 90 95  
 Glu Asp Gln Glu Lys Ile His Ala Leu Thr Ser Glu Asn Thr Asn Leu  
 100 105 110  
 Lys Lys Met Met Ser Asn Gln Tyr Val Pro Val Lys Thr His Glu Glu

115	120	125
Val Lys Met Thr Leu Asn Asp Thr Leu Ala Lys Thr Asn Arg Glu Leu 130 135 140		
Leu Asp Val Lys Lys Lys Phe Glu Asp Ile Asn Gln Glu Phe Val Lys 145 150 155 160		
Ile Lys Asp Lys Asn Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln 165 170 175		
Asn Gln Ile Lys Ala Glu Tyr Ile Ser Leu Ala Glu His Glu Ala Lys 180 185 190		
Met Ser Ser Leu Ser Gln Ser Met Arg Lys Val Gln Asp Ser Asn Ala 195 200 205		
Glu Ile Leu Ala Asn Tyr Arg Lys Gly Gln Glu Glu Ile Val Thr Leu 210 215 220		
His Ala Glu Ile Lys Ala Gln Lys Lys Glu Leu Asp Thr Ile Gln Glu 225 230 235 240		
Cys Ile Lys Val Lys Tyr Ala Pro Ile Val Ser Phe Glu Glu Cys Glu 245 250 255		
Arg Lys Phe Lys Ala Thr Glu Lys Glu Leu Lys Asp Gln Leu Ser Glu 260 265 270		
Gln Thr Gln Lys Tyr Ser Val Ser Glu Glu Glu Val Lys Lys Asn Lys 275 280 285		
Gln Glu Asn Asp Lys Leu Lys Lys Glu Ile Phe Thr Leu Gln Lys Asp 290 295 300		
Leu Arg Asp Lys Thr Val Leu Ile Glu Lys Ser His Glu Met Glu Arg 305 310 315 320		
Ala Leu Ser Arg Lys Thr Asp Glu Leu Asn Lys Gln Leu Lys Asp Leu 325 330 335		
Ser Gln Lys Tyr Thr Glu Val Lys Asn Val Lys Glu Lys Leu Val Glu 340 345 350		
Glu Asn Ala Lys Gln Thr Ser Glu Ile Leu Ala Val Gln Asn Leu Leu 355 360 365		
Gln Lys Gln His Val Pro Leu Glu Gln Val Glu Ala Leu Lys Lys Ser 370 375 380		
Leu Asn Gly Thr Ile Glu Asn Leu Lys Glu Glu Leu Lys Ser Met Gln 385 390 395 400		
Arg Cys Tyr Glu Lys Glu Gln Gln Thr Val Thr Lys Leu His Gln Leu 405 410 415		

Leu Glu Asn Gln Lys Asn Ser Ser Val Pro Leu Ala Glu His Leu Gln  
                             420                            425                            430  
 Ile Lys Glu Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala Ser Leu  
                             435                            440                            445  
 Arg Glu Lys Glu Glu Glu Ser Gln Asn Lys Met Glu Glu Val Ser Lys  
                             450                            455                            460  
 Leu Gln Ser Glu Val Gln Asn Thr Lys Gln Ala Leu Lys Lys Leu Glu  
                             465                            470                            475                            480  
 Thr Arg Glu Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys Ser Asp  
                             485                            490                            495  
 Leu Glu Thr Gln Ile Ser Ser Leu Asn Glu Lys Leu Ala Asn Leu Asn  
                             500                            505                            510  
 Arg Lys Tyr Glu Glu Val Cys Glu Glu Val Leu His Ala Lys Lys Lys  
                             515                            520                            525  
 Glu Ile Ser Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser Ile Glu  
                             530                            535                            540  
 Gln Glu Ile Lys Asp Gln Lys Glu Arg Cys Asp Lys Ser Leu Thr Thr  
                             545                            550                            555                            560  
 Ile Thr Glu Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln Ile Glu  
                             565                            570                            575  
 Ala Lys Asp Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu  
                             580                            585                            590  
 Lys Gln Ala Leu Asn Gly Leu Ser Gln Leu Thr Tyr Thr Ser Gly Asn  
                             595                            600                            605  
 Pro Thr Lys Arg Gln Ser Gln Leu Ile Asp Thr Leu Gln His Gln Val  
                             610                            615                            620  
 Lys Ser Leu Glu Gln Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu  
                             625                            630                            635                            640  
 Val Ile Ala Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln Gly His  
                             645                            650                            655  
 Met Asp Glu Asp Val Gln Glu Ala Leu Leu Gln Ile Ile Gln Met Arg  
                             660                            665                            670  
 Gln Gly Leu Val Cys  
                             675

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2041 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTCCCCCT CCCCACACA CACTCACAGG CCGGGCATTG ATGGTAATGT ATGCGAGGAA	60
ACAGCAGAGA CTCAGTGATG GCTGTCACGA CCGGAGGGGG GACTCGCAGC CTTACCAGGC	120
ACTTAAGTAT TCATCGAAGA GTCACCCAG TAGCGGTGAT CACAGACATG AAAAGATGCG	180
AGACGCCGGA GATCCTTCAC CACCAAATAA AATGTTGCGG AGATCTGATA GTCCTGAAAA	240
CAAATACAGT GACAGCACAG GTCACAGTAA GGCCAAAAAT GTGCATACTC ACAGAGTTAG	300
AGAGAGGGAT GGTGGGACCA GTTACTCTCC ACAAGAAAAT TCACACAACC AAGTGCTCT	360
TCATAGTTCA AATTCACATT CTTCTAATCC AAGCAATAAC CCAAGCAAAA CTTCAGATGC	420
ACCTTATGAT TCTGCAGATG ACTGGTCTGA GCATATTAGC TCTTCTGGGA AAAAGTACTA	480
CTACAATTGT CGAACAGAAG TTTCACAATG GGAAAAACCA AAAGAGTGGC TTGAAAGAGA	540
ACAGAGACAA AAAGAAGCAA ACAAGATGGC AGTCAACAGC TTCCCAAAAG ATAGGGATTA	600
CAGAAGAGAG GTGATGCAAG CAACAGCCAC TAGTGGGTTT GCCAGTGGAA AATCTACATC	660
AGGAGACAAA CCCGTATCAC ATTCTTGAC AACTCCTTCC ACGTCTTCTG CCTCTGGACT	720
GAACCCACAC TCTGCACCTC CAACATCTGC TTCAGCGGTC CCTGTTTCTC CTGTTCCACA	780
GTGCGCAATA CCTCCCTTAC TTCAGGACCC AAATCTTCTT AGACAATTGC TTCCTGCTTT	840
GCAAGCCACG CTGCAGCTTA ATAATCTAA TGTGGACATA TCTAAAATAA ATGAAGTTCT	900
TACAGCAGCT GTGACACAAG CCTCACTGCA GTCTATAATT CATAAGTTTC TTACTGCTGG	960
ACCATCTGCT TTCAACATAA CGTCTCTGAT TTCTCAAGCT GCTCAGCTCT CTACACAAGC	1020
CCAGCCATCT AATCAGTCTC CGATGTCTTT AACATCTGAT GCGTCATCCC CAAGATCATA	1080
TGTTTCTCCA AGAATAAGCA CACCTCAAAC TAACACAGTC CCTATCAAAC CTTTGATCAG	1140
TACTCCTCCT GTTTCATCAC AGCCAAAGGT TAGTACTCCA GTAGTTAAGC AAGGACCAGT	1200
GTCACAGTCA GCCACACAGC AGCCTGTAAC TGCTGACAAG CAGCAAGGTC ATGAACCTGT	1260
CTCTCCTCGA AGTCTTCAGC GCTCAAGCCA GAGAAGTCCA TCACCTGGTC CCAATCATAC	1320

TTCTAATAGT AGTAATGCAT CAAATGCAAC AGTTGTACCA CAGAATTCTT CTGCCCCGATC 1380  
 CACGTGTTCA TTAACGCCTG CACTAGCAGC ACACTTCAGT GAAAATCTCA TAAACACGT 1440  
 TCAAGGATGG CCTGCAGATC ATGCAGAGAA GCAGGCATCA AGATTACGCG AAGAAGCGCA 1500  
 TAACATGGGA ACTATTCA TGTCCGAAAT TTGTACTGAA TTAAAAAATT TAAGATCTTT 1560  
 AGTCCGAGTA TGTGAAATTC AAGCAACTTT GCGAGAGCAA AGGATACTAT TTTTGAGACA 1620  
 ACAAATTAAG GAACTTGAAA AGCTAAAAAA TCAGAATTCC TTCATGGTGT GAAGATGTGA 1680  
 ATAATTGCAC ATGTTTTTGA GAACAGGAAC TGTAATCTG TTGCCCAATC TTAACATTTT 1740  
 TGAGCTGCAT TTAAGTAGAC TTTGGACCGT TAAGCTGGGC AAAGGAAATG ACAAGGGGAC 1800  
 GGGGTCTGTG AGAGTCAATT CAGGGGAAAG ATACAAGATT GATTTGTAAA ACCCTTGAAA 1860  
 TGTAGATTTT TTGTAGATGT ATCCTTCACG TTGTAAATAT GTTTTGTAGA GTGAAGCCAT 1920  
 GGAAGCCAT GTGTAACAGA GCTTAGACAT CCAAACTAA TCAATGCTGA GGTGGCTAAA 1980  
 TACCTAGCCT TTTACATGTA AACCTGTCTG CAAAATTAGC TTTTAAAAA AAAAAAAAAA 2040  
 A 2041

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Gly Asn Ser Arg Asp Ser Val Met Ala Val Thr Thr Gly Gly  
 1 5 10 15  
 Gly Thr Arg Ser Leu Thr Arg His Leu Ser Ile His Arg Arg Val Thr  
 20 25 30  
 Pro Val Ala Val Ile Thr Asp Met Lys Arg Cys Glu Thr Pro Glu Ile  
 35 40 45  
 Leu His His Gln Ile Lys Cys Cys Gly Asp Leu Ile Val Leu Lys Thr  
 50 55 60  
 Asn Thr Val Thr Ala Gln Val Thr Val Arg Pro Lys Met Cys Ile Leu  
 65 70 75 80



Thr Glu Leu Glu Arg Gly Met Val Gly Pro Val Thr Leu His Lys Lys  
 85 90 95  
 Ile His Thr Thr Thr Val Leu Phe Ile Val Gln Ile His Ile Leu Leu  
 100 105 110  
 Ile Gln Ala Ile Thr Gln Ala Lys Leu Gln Met His Leu Met Ile Leu  
 115 120 125  
 Gln Met Thr Gly Leu Ser Ile Leu Ala Leu Leu Gly Lys Ser Thr Thr  
 130 135 140  
 Thr Ile Val Glu Gln Lys Phe His Asn Gly Lys Asn Gln Lys Ser Gly  
 145 150 155 160  
 Leu Lys Glu Asn Arg Asp Lys Lys Lys Gln Thr Arg Trp Gln Ser Thr  
 165 170 175  
 Ala Ser Gln Lys Ile Gly Ile Thr Glu Glu Arg  
 180 185

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCCTATCCA CTTAATAGAT GCCAATTCAA AGAGGTAAAG TGATTAGACT AAGGCACCTA 60  
 ACTTATGTGA GTGTCAGGCT TCAATGCCTG TGTTAGAGCT ACTCCTTCAC ACAAATAGT 120  
 TCAGAACATA GAGAAGGACC AAGGTTAATA AATGATTTTC ATCCCAAACA CTAAACATGA 180  
 TTGATGGGTA GAGGCTGCCC GAAGTACTGT GTAAAGATGG AATCTGAGAT AGAAGAATGC 240  
 TGTGGTCAAT TAGTAATTCT TGCCCATGGA GGGATTAGTG ACACATGCCT TGTATATTTG 300  
 TCATCTGTGG CCTAAACTCT GCCCCTGAAG GTTTGTTTTC TAATTCAGAG GTTTAAATTA 360  
 ATCTAGCCCA CTTAATAAAA CCAGAGATCC TATGGGAAAT TTAGCCTAAG ACAGTGCTGG 420  
 AAATTGCCAT ATGTTGATAC AAAGAAGTGT TTGGCCACAT TACAGGTCTC AGACTCAACT 480  
 GCTATGTGTG ACTGCCGCTC TGTGCCTATG TCTTGCTTTT TTGCTGAGTT CCCTATTTCC 540  
 ATATCTCCAG GTGAATCCAT GAGAAGCGAG AGGGTGGCTG AGAGGCCTGG GCCTCTGGGA 600

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TTCCACCTTG CTATCTCTGC TCTTCAACCA TTGTTT TAGA CTCTGAACAC CAGATCCTCA      660
TATCTGAAAG TGATTTGGAG ACCTGGGCAT CAAGTGCTCT TTTAAGAAGG GGCTATCCCA      720
GAGGACTGTT CAAAAGTCTC ATTCAATAGA GATGTTGGAG TCCCAGAACA AAGTTAGGGA      780
GCAAACCACT AACCTATGCT GGTSGTAACA GAGGATCCTA CAATTACGTT TGTTTTAAAG      840
ACAGGATTTT GCTGTGTTGC CCAGACTGGT CTCAAACCTCC TGGGTTC AAG AGATCCATCC      900
TCCCACCTCA GTCTCCTGAA AGCTGGGATG ACAGGCACAT GCCACCACAC CTAGCTCCTT      960
ACAACCATTT ATTTTAACTT ATTTTCATTTA TAACTGGTAT CTTTCATTTG TATGTGGCAG     1020
CTAGAGATTT ATATAGGATG GAAGTAATTT ATTTTAAATT TAAATATTTT ATGTTGAACT     1080
GTTTGCCTTG TATGGAACAT TTTACTTGGC CAATTCAAAT AAAAATAAAG TCAGCTTTGT     1140
TTGTGACAAA AAAAAAAAAA AAA                                     1163

```

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Leu Ile Gln Arg Ser Val Trp Pro His Tyr Arg Ser Gln Thr Gln
1           5           10           15
Leu Leu Cys Val Thr Ala Ala Leu Cys Leu Cys Leu Ala Phe Leu Leu
          20           25           30
Ser Ser Leu Phe Pro Tyr Leu Gln Val Asn Pro
          35           40

```

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3067 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGGTGGCTG AGGCGGCTGG GCCTAGGGTG CAGCGGGCGC GTCTGCGGCT GGTGTTGGCG	60
CATCTCTAGA TCCTTTCCCG GAGTTCAGTT ATGGGTGTGA GAGGTTTGCA AGGATTTGTG	120
GGAAGTACCT GCCACATAT ATGTACAGTA GTAAATTTCA AAGAACTGGC AGAGCACCAC	180
CGAAGCAAGT ATCCTGGATG TACCCCTACC ATTGTGGTTG ATGCCATGTG TTGTCTCAGA	240
TATTGGTATA CTCCAGAATC TTGGATCTGC GTTGCCAGT GCGGAGAATA CTTTCTGCT	300
TTGCGAGATT TTGTTAAAC TTTTACGGCA GCTGGGATCA AGTTGATATT CTCTTTGAT	360
GGCATGGTGG AGCAGGATAA GAGAGATGAA TGGGTGAAAC GAAGGCTCAA GAACAACAGG	420
GAGATATCCA GGATTTTCA TTACATCAAG TCACACAAGG AGCAGCCAGG CAGAAATATG	480
TTCTTCATCC CCTCAGGGCT AGCTGTGTTT ACACGATTTG CTCTAAAGAC ACTGGGCCAG	540
GAAACTTTGT GTTCTTTGCA GGAAGCAGAT TATGAGGTAG CTTCTATGG CCTCCAGCAT	600
AACTGTCTTG GGATTCTGGG GGAAGACACT GATTACCTAA TCTATGACAC TTGTCCCTAC	660
TTTTCAATTA GCGAGCTCTG CCTAGAGAGC CTGGACACCG TCATGCTCTG CAGAGAGAAG	720
CTCTGTGAGA GTCTGGGCCT CTGTGTGGCC GACCTTCCTC TTCTGGCCTG CCTCCTGGC	780
GACGACATAA TCCCAGAGGG CATGTTTGAA AGCTTTAGGT ACAAATGCTT ATCGTCCTAC	840
ACCTCTGTAA AAGAGAACTT TGACAAAAA GGTAACATCA TATTAGCTGT GTCAGACCAT	900
ATATCGAAAG TTCTTTACTT GTATCAAGGT GAGAAAAAAT TAGAAGAGAT ATTACCTCTG	960
GGACCAAACA AAGCTCTTTT TTATAAAGGA ATGGCATCAT ATCTTTTACC AGGACAAAAA	1020
TCTCCATGGT TTTTCCAAAA ACCCAAAGGT GTAATAACTT TGGACAAACA AGTAATATCC	1080
ACGAGTTCAG ACGCCGAATC CAGGGAAGAA GTTCCCATGT GTTCAGATGC TGAATCCAGG	1140
CAAGAAGTTC CCATGTGTAC AGGCCCTGAA TCCAGGCGAG AAGTTCCCGT GTATACAGAT	1200
TCTGAACCCA GGCAAGAAGT TCCCATGTGT TCAGACCCTG AACCCAGGCA AGAAGTTCCC	1260
ACATGTACAG GCCCTGAATC CAGGCGAGAA GTTCCCATGT GTTCAGACCC TGAACCCAGG	1320
CAAGAAGTTC CCATGTGTAC AGGCCCTGAA GCCAGGCAAG AAGTTCCCAT GTATACAGAC	1380
TCTGAACCCA GGCAAGAAGT TCCCATGTAT ACAGACTCTG AACCCAGGCA AGAAGTTCCC	1440
ATGTATACAG GCTCTGAACC CAGGCAAGAA GTTCCCATGT ATACAGGCCC TGAATCCAGG	1500
CAAGAAGTTC CCATGTATAC AGGCCCTGAA TCCAGGCAAG AAGTTTAAAT ACGGACAGAC	1560

CCTGAATCTA GGCAAGAAAT TATGTGTACA GGCCATGAAT CCAAACAGGA AGTTCCCATATA	1620
TGTACAGATC CTATATCCAA GCAAGAAGAC TCCATGTGTA CACACGCTGA AATCAATCAA	1680
AAATTACCTG TAGCAACAGA TTTTGAATTT AAGCTAGAAG CTCTCATGTG TACAAACCCT	1740
GAAATTAAAC AAGAAGACCC CACAAATGTG GGCCTGAAG TAAAGCAACA AGTAACCATG	1800
GTTCAGACA CTGAAATCTT AAAGGTTGCT AGAACACATC ACGTCCAAGC AGAAAGCTAC	1860
CTGGTGTACA ACATCATGAG CAGTGGAGAG ATTGAATGCA GCAACACCCT AGAAGATGAG	1920
CTTGACCAGG CCTTACCCAG CCAGGCCTTC ATTTACCGTC CCATTGACA GCGGGTCTAC	1980
TCACTCTTAC TGGAGGACTG TCAAGATGTC ACCAGCACCT GCCTAGCTGT CAAGGAGTGG	2040
TTTGTGTATC CTGGGAACCC ACTGAGGCAC CCGGACCTCG TCAGGCCGCT GCAGATGACC	2100
ATTCCAGGGG GAACGCCTAG TTTGAAAATA TTATGGCTGA ACCAAGAGCC AGAAATACAG	2160
GTTCGGCGCT TGGACACACT CCTAGCCTGT TTCAATCTTT CCTCCTCAAG AGAAGAGCTG	2220
CAGGCTGTG AAAGCCCAT TCAAGCTTTG TGCTGCCTCT TGATCTACCT CTTTGTCCAG	2280
GTGGACACGC TTTGCCTGGA GGATTTGCAT GCGTTTATTG CGCAGGCCTT GTGCCTCCAA	2340
GGAAAATCCA CCTCGCAGCT TGTAATCTA CAGCCTGATT ACATCAACCC CAGAGCCGTG	2400
CAGCTGGGCT CCCTTCTCGT CCGCGGCCTC ACCACTCTGG TTTTAGTCAA CAGCGCATGT	2460
GGCTTCCCCT GGAAGACGAG TGATTTTCATG CCCTGGAATG TATTTGACGG GAAGCTTTTT	2520
CATCAGAAGT ACTTGCAATC TGAAAAGGGT TATGCTGTGG AGGTTCTTTT AGAACAAAAT	2580
GGAGGTGGGG AAGACAGGGC TCCAGCTACC ACAGGACGGG CTCTGGGTAT AGCCGTTCOA	2640
GTCAGGGACA GCCGTGGAGA GACCAGGGAC CAGGAAGCAG ACAGTATGAG CATGACCAGT	2700
GGAGAAGGTA CTAGTCAACC TCCAGAAAGA GTATGGAGAG AAAAAGAGGC ACACCTGGAC	2760
GCAGAGCCCT GCCAGCGCCC TCCTCTGCTG TTGCAGCTGC AAGGAGACCA TGCCTGTGGG	2820
AGCCAGGCCT CGCTTGCATG AAGAAGGAAC GATGCCTTTT TCAATGGTGT CTCCCTCCCA	2880
TTGTGCAGAA GAGCTTTTGT TGGCTTCTCT CCCGAGCTTG TGCTGATTC TGTGGCCCAA	2940
AACAATCATT GTTAACATCT TCATGTGTTT CATTCGTATC TTTCATTCAT ATATATGATG	3000
CCTAGCTAAT TTCATTTTAA AATAAATGGG AATCTGTTGT AAAAAAAAAA AAAAAAAAAA	3060
AAAAAA	3067

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 916 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Gly Val Arg Gly Leu Gln Gly Phe Val Gly Ser Thr Cys Pro His
1           5           10           15

Ile Cys Thr Val Val Asn Phe Lys Glu Leu Ala Glu His His Arg Ser
20           25           30

Lys Tyr Pro Gly Cys Thr Pro Thr Ile Val Val Asp Ala Met Cys Cys
35           40           45

Leu Arg Tyr Trp Tyr Thr Pro Glu Ser Trp Ile Cys Gly Gly Gln Trp
50           55           60

Arg Glu Tyr Phe Ser Ala Leu Arg Asp Phe Val Lys Thr Phe Thr Ala
65           70           75           80

Ala Gly Ile Lys Leu Ile Phe Phe Phe Asp Gly Met Val Glu Gln Asp
85           90           95

Lys Arg Asp Glu Trp Val Lys Arg Arg Leu Lys Asn Asn Arg Glu Ile
100          105          110

Ser Arg Ile Phe His Tyr Ile Lys Ser His Lys Glu Gln Pro Gly Arg
115          120          125

Asn Met Phe Phe Ile Pro Ser Gly Leu Ala Val Phe Thr Arg Phe Ala
130          135          140

Leu Lys Thr Leu Gly Gln Glu Thr Leu Cys Ser Leu Gln Glu Ala Asp
145          150          155          160

Tyr Glu Val Ala Ser Tyr Gly Leu Gln His Asn Cys Leu Gly Ile Leu
165          170          175

Gly Glu Asp Thr Asp Tyr Leu Ile Tyr Asp Thr Cys Pro Tyr Phe Ser
180          185          190

Ile Ser Glu Leu Cys Leu Glu Ser Leu Asp Thr Val Met Leu Cys Arg
195          200          205

Glu Lys Leu Cys Glu Ser Leu Gly Leu Cys Val Ala Asp Leu Pro Leu
210          215          220

Leu Ala Cys Leu Leu Gly Asp Asp Ile Ile Pro Glu Gly Met Phe Glu

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225                      230                      235                      240  
 Ser Phe Arg Tyr Lys Cys Leu Ser Ser Tyr Thr Ser Val Lys Glu Asn  
                                  245                      250                      255  
 Phe Asp Lys Lys Gly Asn Ile Ile Leu Ala Val Ser Asp His Ile Ser  
                                  260                      265                      270  
 Lys Val Leu Tyr Leu Tyr Gln Gly Glu Lys Lys Leu Glu Glu Ile Leu  
                                  275                      280                      285  
 Pro Leu Gly Pro Asn Lys Ala Leu Phe Tyr Lys Gly Met Ala Ser Tyr  
                                  290                      295                      300  
 Leu Leu Pro Gly Gln Lys Ser Pro Trp Phe Phe Gln Lys Pro Lys Gly  
 305                                   310                      315                      320  
 Val Ile Thr Leu Asp Lys Gln Val Ile Ser Thr Ser Ser Asp Ala Glu  
                                  325                      330                      335  
 Ser Arg Glu Glu Val Pro Met Cys Ser Asp Ala Glu Ser Arg Gln Glu  
                                  340                      345                      350  
 Val Pro Met Cys Thr Gly Pro Glu Ser Arg Arg Glu Val Pro Val Tyr  
                                  355                      360                      365  
 Thr Asp Ser Glu Pro Arg Gln Glu Val Pro Met Cys Ser Asp Pro Glu  
                                  370                      375                      380  
 Pro Arg Gln Glu Val Pro Thr Cys Thr Gly Pro Glu Ser Arg Arg Glu  
 385                                   390                      395                      400  
 Val Pro Met Cys Ser Asp Pro Glu Pro Arg Gln Glu Val Pro Met Cys  
                                  405                      410                      415  
 Thr Gly Pro Glu Ala Arg Gln Glu Val Pro Met Tyr Thr Asp Ser Glu  
                                  420                      425                      430  
 Pro Arg Gln Glu Val Pro Met Tyr Thr Asp Ser Glu Pro Arg Gln Glu  
                                  435                      440                      445  
 Val Pro Met Tyr Thr Gly Ser Glu Pro Arg Gln Glu Val Pro Met Tyr  
                                  450                      455                      460  
 Thr Gly Pro Glu Ser Arg Gln Glu Val Pro Met Tyr Thr Gly Pro Glu  
 465                                   470                      475                      480  
 Ser Arg Gln Glu Val Leu Ile Arg Thr Asp Pro Glu Ser Arg Gln Glu  
                                  485                      490                      495  
 Ile Met Cys Thr Gly His Glu Ser Lys Gln Glu Val Pro Ile Cys Thr  
                                  500                      505                      510  
 Asp Pro Ile Ser Lys Gln Glu Asp Ser Met Cys Thr His Ala Glu Ile  
                                  515                      520                      525

Asn Gln Lys Leu Pro Val Ala Thr Asp Phe Glu Phe Lys Leu Glu Ala  
 530 535 540  
 Leu Met Cys Thr Asn Pro Glu Ile Lys Gln Glu Asp Pro Thr Asn Val  
 545 550 555 560  
 Gly Pro Glu Val Lys Gln Gln Val Thr Met Val Ser Asp Thr Glu Ile  
 565 570 575  
 Leu Lys Val Ala Arg Thr His His Val Gln Ala Glu Ser Tyr Leu Val  
 580 585 590  
 Tyr Asn Ile Met Ser Ser Gly Glu Ile Glu Cys Ser Asn Thr Leu Glu  
 595 600 605  
 Asp Glu Leu Asp Gln Ala Leu Pro Ser Gln Ala Phe Ile Tyr Arg Pro  
 610 615 620  
 Ile Arg Gln Arg Val Tyr Ser Leu Leu Leu Glu Asp Cys Gln Asp Val  
 625 630 635 640  
 Thr Ser Thr Cys Leu Ala Val Lys Glu Trp Phe Val Tyr Pro Gly Asn  
 645 650 655  
 Pro Leu Arg His Pro Asp Leu Val Arg Pro Leu Gln Met Thr Ile Pro  
 660 665 670  
 Gly Gly Thr Pro Ser Leu Lys Ile Leu Trp Leu Asn Gln Glu Pro Glu  
 675 680 685  
 Ile Gln Val Arg Arg Leu Asp Thr Leu Leu Ala Cys Phe Asn Leu Ser  
 690 695 700  
 Ser Ser Arg Glu Glu Leu Gln Ala Val Glu Ser Pro Phe Gln Ala Leu  
 705 710 715 720  
 Cys Cys Leu Leu Ile Tyr Leu Phe Val Gln Val Asp Thr Leu Cys Leu  
 725 730 735  
 Glu Asp Leu His Ala Phe Ile Ala Gln Ala Leu Cys Leu Gln Gly Lys  
 740 745 750  
 Ser Thr Ser Gln Leu Val Asn Leu Gln Pro Asp Tyr Ile Asn Pro Arg  
 755 760 765  
 Ala Val Gln Leu Gly Ser Leu Leu Val Arg Gly Leu Thr Thr Leu Val  
 770 775 780  
 Leu Val Asn Ser Ala Cys Gly Phe Pro Trp Lys Thr Ser Asp Phe Met  
 785 790 795 800  
 Pro Trp Asn Val Phe Asp Gly Lys Leu Phe His Gln Lys Tyr Leu Gln  
 805 810 815  
 Ser Glu Lys Gly Tyr Ala Val Glu Val Leu Leu Glu Gln Asn Gly Gly

	820		825		830										
Gly	Glu	Asp	Arg	Ala	Pro	Ala	Thr	Thr	Gly	Arg	Ala	Leu	Gly	Ile	Ala
	835						840					845			
Val	Pro	Val	Arg	Asp	Ser	Arg	Gly	Glu	Thr	Arg	Asp	Gln	Glu	Ala	Asp
	850					855					860				
Ser	Met	Ser	Met	Thr	Ser	Gly	Glu	Gly	Thr	Ser	Gln	Pro	Pro	Glu	Arg
865					870					875					880
Val	Trp	Arg	Glu	Lys	Glu	Ala	His	Leu	Asp	Ala	Glu	Pro	Cys	Gln	Arg
			885						890					895	
Pro	Pro	Leu	Leu	Leu	Gln	Leu	Gln	Gly	Asp	His	Ala	Cys	Gly	Ser	Gln
		900						905					910		
Ala	Ser	Leu	Ala												
		915													

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1914 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTGTCTGC TCTCCTGGCA GGAATCGCTG AGGGAGGGAA ACGCGGCTCT GAATCAGCCC	60
AGAACGAGCC TTCGGGAAGC TCACCCTCCG ATCTCGGTGT GATTGTTGTG ATTGTTGTGA	120
TTTCCTGTCT CGTTTGCCTT GACCGCCATG TGAAAGAATC TGTTCCTCCAG CTAGGTGGGG	180
AAAATTCACA GGTGGGCTGT CTGTAGAGAG AACTGGCTGA TTAAAGGCTT CTCGTCCCGA	240
TTTTGTGATA GCCAAGTGCT TGGCCTGGTC GACGGTCTTT GCTCCTTTAC AAATAAAGTG	300
TTCTGTTTCA GTTCGTCCCA AGTTTTCAT GAAGGGCAGT GGTTCCTGA CCTCCCAGGT	360
GCCTGGGCTT CCCAGGTTT CTGATCTGGG GCTTGGGGCC CTGTGTTTGG GGATCGTGGC	420
ACTGTGTGCA CCAGCCTGGA AGCACTGGGC CAGTCTTGGC CAAGCTTTCC ATCAGGGATG	480
ATTTGATCTT GGTGCTACAG GTCTGTGGTA CGACCATTGT TCCACACCAC ATGTCATTAA	540
TAATGCTTCC CATGCTTCTG CTTGCAAATG ACCAGCCTTC CAAACAGCCA GAGCTGTTTC	600



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GAGGTGTTTC TGCAGGCAGG TGCAGGCGTG CCCTCAAATA AGCTTTGCCA ATGGAGTCTC      660
AGCAAGAGCA AAACCTGGTC AGGAAAGACA AAGCCTGGGA ATCCACCCCC ATGCCCTGCA      720
GGTTGGCTGG CCCTGGAGCC ATTTATTATA GTGCTAATCA TGTTCCTAGG CAGGTGCAGA      780
TGGCAAGGGC AGTGTCTTGG TGAGCTTTTT AGCACGAAGA GCCAGGTCTG TCGAAGCCTT      840
TGTGAGAGCT GGAAACGCAG GTGTGCTGGG CATGCGCAGT ATGGGGTTTC GGGCTCAGGG      900
CTTGCCCTTT GGCATCAGAC AGACCTGGCT TCGCATCCTG GATTGCTTC TGACGTGCAC      960
CCTTCCCTTT GGGTCTCGTG ATGTGAAATG GAGATGTTGT CATTTGTGAG GGCTCCATGA     1020
AGTTTCGTTG AAATGACAAA TACTAATTTC TTCATCTGTG AAATGGAGAT AATAGTGTG     1080
ACCTCAGAAC AGCTGAGAGG ACTAAATGAA ATGATGTTGG ATGTAGCCAT AAAGAACGAA     1140
GTCAGGCACT GGTGCACGCC TGGAATCCCA GCTCTTGGGA GACCGAGACA GGTGGATTGC     1200
TTGAGCTCAG GAGTTTGAGA CCAGCCTGAG CAACATAGGG AGGTCCAGTC TCTACAAAAA     1260
ATATGAAAAG TAGCTGGGCG TGGTGGCGCA TGCCTGTAGT CCCACTACTT GGAAGGCTTC     1320
GTTGGGAGGA TCACCTGAGC CCAGAAGATT GAGGCTGCAG TAAGCCGTGA TCGTGCCACT     1380
GCATTCCAGC CTGGGCAACA GAGCGAGACA CTGTCTCAAA TAAAAAAGAT GGAATAGTA     1440
GACACTGGGG GCTCCAGAAG GAGGGAGGGA GGGAGGAAGG GGAGGAAGGG CTGAAATGCT     1500
TTCTATTGGA TACTATCTGG GCATATTACT TCCTGTGGTT CACTGTCTGG GTGACAGGAT     1560
TCATAGAAGC CCAAACTTTA GCACCACGCA GCATACCCCT GTAACAAAGC CGCACACGTA     1620
CGCCCTCAAG CTAAAACAAA AGTGGACCGG GAGGCCGAGG TCGGGGGATC ATGAGGTCAG     1680
GAGTTTGAGA CCAGCCTGGC AGATAACGGT GAAACCCCGT CTCTACTAAA AATACCAAAA     1740
AAAGTTAGCC GGACATGGTG GCAGGTGCCT GTAGTCCCAG CTACTTGGGA GGCTGGGGCA     1800
GAAGAATCGC TTGAACCCAG GAGGCGGAGG TTGCAGTGAG CCGAGATTGC GCCACTGCAC     1860
TCCAGCCTGT GCGACAGAGT GAGACTCCGT CTCAAAAAAA AAAAAAAAAA AAAA          1914

```

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 137 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met Thr Ser Leu Pro Asn Ser Gln Ser Cys Phe Glu Val Phe Leu Gln
1           5           10           15

Ala Gly Ala Gly Val Pro Ser Asn Lys Leu Cys Gln Trp Ser Leu Ser
          20           25           30

Lys Ser Lys Thr Trp Ser Gly Lys Thr Lys Pro Gly Asn Pro Pro Pro
          35           40           45

Cys Pro Ala Gly Trp Leu Ala Leu Glu Pro Phe Ile Ile Val Leu Ile
          50           55           60

Met Phe Leu Gly Arg Cys Arg Trp Gln Gly Gln Cys Leu Gly Glu Leu
65           70           75           80

Phe Ser Thr Lys Ser Gln Val Cys Arg Ser Leu Cys Glu Ser Trp Lys
          85           90           95

Arg Arg Cys Ala Gly His Ala Gln Tyr Gly Val Ser Gly Ser Gly Leu
          100          105          110

Ala Leu Trp His Gln Thr Asp Leu Ala Ser His Pro Gly Phe Ala Ser
          115          120          125

Asp Val His Pro Ser Leu Trp Val Ser
          130          135

```

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

CCGACTCCCT TCTTTATGGC GTCGCTCCTG TGCTGTGGGC CGAAGCTGGC CGCCTGCGGC      60
ATCGTCCTCA GCGCCTGGGG AGTGATCATG TTGATAATGC TCGGAATATT TTTCAATGTC      120
CATTCGCTG TGTGATTGA GGACGTTCCC TTCACGGAGA AAGATTTTGA GAATGGCCCC      180
CAGAACATAT ACAACCTTTA CGAGCAAGTC AGCTACAAC TTTTCATCGC TGCAGGCCTT      240
TACCTCCTCC TCGGAGGCTT CTCTTTCTGC CAAGTTCGGC TCAATAAGCG CAAGGAATAC      300

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```

ATGGTGCCT AGGGCCCCGG CGCGTTTCCC CGCTCCAGCC CCTCCTCTAT TTAAAGACTC   360
CCTGCACCGT GTCACCCAGG TCGCGTCCCA CCCTTGCCGG CGCCCTCTGT GGGACTGGGT   420
TTCCCGGGCG AGAGACTGAA TCCCTTCTCC CATCTCTGGC ATCCGGCCCC CGTGGAGAGG   480
GCTGAGGCTG GGGGGCTGTT CCGTCTCTCC ACCCTTCGCT GTGTCCCGTA TCTCAATAAA   540
GAGAATCTGC TCTCTTCAAA AAAAAAAAAA AAAAA                               575

```

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
1           5           10           15
Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
20          25          30
Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
35          40          45
Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln
50          55          60
Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
65          70          75          80
Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met
85          90          95
Val Arg

```

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GNAGCCCAGGA GTCTTCTCAA CCTCTTCC

29

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ANCAGTCGCAA GTGCATAGTA ACCCAGTA

29

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TNCTCAGCTTT TATTTGGTTC TGAGTGTT

29

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TNTGCTCAGAC CAGTCATCTG CAGAATCA

29

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TNCAGCACTGT CTTAGGCTAA ATTTCCCA

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GNATTCGGCGT CTGAACTCGT GGATATTA

29

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ANATGCCCAGA TAGTATCCAA TAGAAAGC

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CNACAGCACAG GAGCGACGCC ATAAAGAA

29

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Val Met Tyr Ala Arg Lys Gln Gln Arg Leu Ser Asp Gly Cys His  
1 5 10 15

Asp Arg Arg Gly Asp Ser Gln Pro Tyr Gln Ala Leu Lys Tyr Ser Ser  
20 25 30

Lys Ser His Pro Ser Ser Gly Asp His Arg His Glu Lys Met Arg Asp  
35 40 45

Ala Gly Asp Pro Ser Pro Pro Asn Lys Met Leu Arg Arg Ser Asp Ser  
50 55 60

Pro Glu Asn Lys Tyr Ser Asp Ser Thr Gly His Ser Lys Ala Lys Asn  
65 70 75 80

Val His Thr His Arg Val Arg Glu Arg Asp Gly Gly Thr Ser Tyr Ser  
85 90 95

Pro Gln Glu Asn Ser His Asn His Ser Ala Leu His Ser Ser Asn Ser  
 100 105 110  
 His Ser Ser Asn Pro Ser Asn Asn Pro Ser Lys Thr Ser Asp Ala Pro  
 115 120 125  
 Tyr Asp Ser Ala Asp Asp Trp Ser Glu His Ile Ser Ser Ser Gly Lys  
 130 135 140  
 Lys Tyr Tyr Tyr Asn Cys Arg Thr Glu Val Ser Gln Trp Glu Lys Pro  
 145 150 155 160  
 Lys Glu Trp Leu Glu Arg Glu Gln Arg Gln Lys Glu Ala Asn Lys Met  
 165 170 175  
 Ala Val Asn Ser Phe Pro Lys Asp Arg Asp Tyr Arg Arg Glu Val Met  
 180 185 190  
 Gln Ala Thr Ala Thr Ser Gly Phe Ala Ser Gly Lys Ser Thr Ser Gly  
 195 200 205  
 Asp Lys Pro Val Ser His Ser Cys Thr Thr Pro Ser Thr Ser Ser Ala  
 210 215 220  
 Ser Gly Leu Asn Pro Thr Ser Ala Pro Pro Thr Ser Ala Ser Ala Val  
 225 230 235 240  
 Pro Val Ser Pro Val Pro Gln Ser Pro Ile Pro Pro Leu Leu Gln Asp  
 245 250 255  
 Pro Asn Leu Leu Arg Gln Leu Leu Pro Ala Leu Gln Ala Thr Leu Gln  
 260 265 270  
 Leu Asn Asn Ser Asn Val Asp Ile Ser Lys Ile Asn Glu Val Leu Thr  
 275 280 285  
 Ala Ala Val Thr Gln Ala Ser Leu Gln Ser Ile Ile His Lys Phe Leu  
 290 295 300  
 Thr Ala Gly Pro Ser Ala Phe Asn Ile Thr Ser Leu Ile Ser Gln Ala  
 305 310 315 320  
 Ala Gln Leu Ser Thr Gln Ala Gln Pro Ser Asn Gln Ser Pro Met Ser  
 325 330 335  
 Leu Thr Ser Asp Ala Ser Ser Pro Arg Ser Tyr Val Ser Pro Arg Ile  
 340 345 350  
 Ser Thr Pro Gln Thr Asn Thr Val Pro Ile Lys Pro Leu Ile Ser Thr  
 355 360 365  
 Pro Pro Val Ser Ser Gln Pro Lys Val Ser Thr Pro Val Val Lys Gln  
 370 375 380  
 Gly Pro Val Ser Gln Ser Ala Thr Gln Gln Pro Val Thr Ala Asp Lys

385		390		395		400
Gln Gln Gly His Glu Pro Val Ser Pro Arg Ser Leu Gln Arg Ser Ser						
	405			410		415
Gln Arg Ser Pro Ser Pro Gly Pro Asn His Thr Ser Asn Ser Ser Asn						
	420		425			430
Ala Ser Asn Ala Thr Val Val Pro Gln Asn Ser Ser Ala Arg Ser Thr						
	435		440			445
Cys Ser Leu Thr Pro Ala Leu Ala Ala His Phe Ser Glu Asn Leu Ile						
	450		455			460
Lys His Val Gln Gly Trp Pro Ala Asp His Ala Glu Lys Gln Ala Ser						
	465		470		475	480
Arg Leu Arg Glu Glu Ala His Asn Met Gly Thr Ile His Met Ser Glu						
		485		490		495
Ile Cys Thr Glu Leu Lys Asn Leu Arg Ser Leu Val Arg Val Cys Glu						
	500		505			510
Ile Gln Ala Thr Leu Arg Glu Gln Arg Ile Leu Phe Leu Arg Gln Gln						
	515		520			525
Ile Lys Glu Leu Glu Lys Leu Lys Asn Gln Asn Ser Phe Met Val						
	530		535			540



What is claimed is:

1. An isolated polynucleotide selected from the group consisting of:
  - (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 99 to nucleotide 902;
  - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 162 to nucleotide 902;
  - (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 219;
  - (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ci25\_4 deposited under accession number ATCC 98415;
  - (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ci25\_4 deposited under accession number ATCC 98415;
  - (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ci25\_4 deposited under accession number ATCC 98415;
  - (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ci25\_4 deposited under accession number ATCC 98415;
  - (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
  - (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:2;
  - (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
  - (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
  - (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j).

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:
  - (a) growing a culture of the host cell of claim 3 in a suitable culture medium; and
  - (b) purifying said protein from the culture.
6. A protein produced according to the process of claim 5.
7. The protein of claim 6 comprising a mature protein.
8. A protein comprising an amino acid sequence selected from the group consisting of:
  - (a) the amino acid sequence of SEQ ID NO:2;
  - (b) fragments of the amino acid sequence of SEQ ID NO:2 comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:2; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ci25\_4 deposited under accession number ATCC 98415;the protein being substantially free from other mammalian proteins.
9. The protein of claim 8, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.
10. A composition comprising the protein of claim 8 and a pharmaceutically acceptable carrier.
11. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:1.

12. An isolated polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 283 to nucleotide 1158;
  - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 1 to nucleotide 789;
  - (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone da228\_6 deposited under accession number ATCC 98415;
  - (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone da228\_6 deposited under accession number ATCC 98415;
  - (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone da228\_6 deposited under accession number ATCC 98415;
  - (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone da228\_6 deposited under accession number ATCC 98415;
  - (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
  - (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 141 to amino acid 150 of SEQ ID NO:4;
  - (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
  - (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
  - (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).
13. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:4;

- (b) the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 169;
  - (c) fragments of the amino acid sequence of SEQ ID NO:4 comprising the amino acid sequence from amino acid 141 to amino acid 150 of SEQ ID NO:4; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone da228\_6 deposited under accession number ATCC 98415;
- the protein being substantially free from other mammalian proteins.

14. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:3.
15. An isolated polynucleotide selected from the group consisting of:
  - (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 152 to nucleotide 2182;
  - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 2 to nucleotide 931;
  - (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone du410\_5 deposited under accession number ATCC 98415;
  - (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone du410\_5 deposited under accession number ATCC 98415;
  - (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone du410\_5 deposited under accession number ATCC 98415;
  - (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone du410\_5 deposited under accession number ATCC 98415;
  - (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
  - (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 333 to amino acid 342 of SEQ ID NO:6;

- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

16. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
- (b) the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 260;
- (c) fragments of the amino acid sequence of SEQ ID NO:6 comprising the amino acid sequence from amino acid 333 to amino acid 342 of SEQ ID NO:6; and
- (d) the amino acid sequence encoded by the cDNA insert of clone du410\_5 deposited under accession number ATCC 98415;

the protein being substantially free from other mammalian proteins.

17. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:5.

18. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 51 to nucleotide 611;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 1 to nucleotide 525;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone eh80\_1 deposited under accession number ATCC 98415;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone eh80\_1 deposited under accession number ATCC 98415;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone eh80\_1 deposited under accession number ATCC 98415;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone eh80\_1 deposited under accession number ATCC 98415;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 88 to amino acid 97 of SEQ ID NO:8;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

19. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:8;

(b) the amino acid sequence of SEQ ID NO:8 from amino acid 1 to amino acid 158;

(c) fragments of the amino acid sequence of SEQ ID NO:8 comprising the amino acid sequence from amino acid 88 to amino acid 97 of SEQ ID NO:8; and

(d) the amino acid sequence encoded by the cDNA insert of clone eh80\_1 deposited under accession number ATCC 98415;

the protein being substantially free from other mammalian proteins.

20. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:7.

21. An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 431 to nucleotide 559;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 518 to nucleotide 559;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 190 to nucleotide 547;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone er369\_1 deposited under accession number ATCC 98415;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone er369\_1 deposited under accession number ATCC 98415;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone er369\_1 deposited under accession number ATCC 98415;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone er369\_1 deposited under accession number ATCC 98415;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 16 to amino acid 25 of SEQ ID NO:10;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j).

22. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) the amino acid sequence of SEQ ID NO:10 from amino acid 1 to amino acid 39;

- (c) fragments of the amino acid sequence of SEQ ID NO:10 comprising the amino acid sequence from amino acid 16 to amino acid 25 of SEQ ID NO:10; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone er369\_1 deposited under accession number ATCC 98415;
- the protein being substantially free from other mammalian proteins.

23. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:9.
24. An isolated polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 91 to nucleotide 2838;
  - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 2209 to nucleotide 2838;
  - (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 839 to nucleotide 1197;
  - (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fh123\_5 deposited under accession number ATCC 98415;
  - (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fh123\_5 deposited under accession number ATCC 98415;
  - (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fh123\_5 deposited under accession number ATCC 98415;
  - (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fh123\_5 deposited under accession number ATCC 98415;
  - (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
  - (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 453 to amino acid 462 of SEQ ID NO:12;



- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j).

25. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
- (b) the amino acid sequence of SEQ ID NO:12 from amino acid 251 to amino acid 369;
- (c) fragments of the amino acid sequence of SEQ ID NO:12 comprising the amino acid sequence from amino acid 453 to amino acid 462 of SEQ ID NO:12; and
- (d) the amino acid sequence encoded by the cDNA insert of clone fh123\_5 deposited under accession number ATCC 98415;

the protein being substantially free from other mammalian proteins.

26. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:11.

27. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 568 to nucleotide 978;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 1084 to nucleotide 1854;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fm60\_1 deposited under accession number ATCC 98415;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fm60\_1 deposited under accession number ATCC 98415;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fm60\_1 deposited under accession number ATCC 98415;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fm60\_1 deposited under accession number ATCC 98415;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:14;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

28. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:14;

(b) fragments of the amino acid sequence of SEQ ID NO:14 comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:14; and

(c) the amino acid sequence encoded by the cDNA insert of clone fm60\_1 deposited under accession number ATCC 98415;

the protein being substantially free from other mammalian proteins.

29. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:13.

30. An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 16 to nucleotide 309;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 127 to nucleotide 309;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fr473\_2 deposited under accession number ATCC 98415;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fr473\_2 deposited under accession number ATCC 98415;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fr473\_2 deposited under accession number ATCC 98415;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fr473\_2 deposited under accession number ATCC 98415;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:16;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

31. A protein comprising an amino acid sequence selected from the group consisting of:

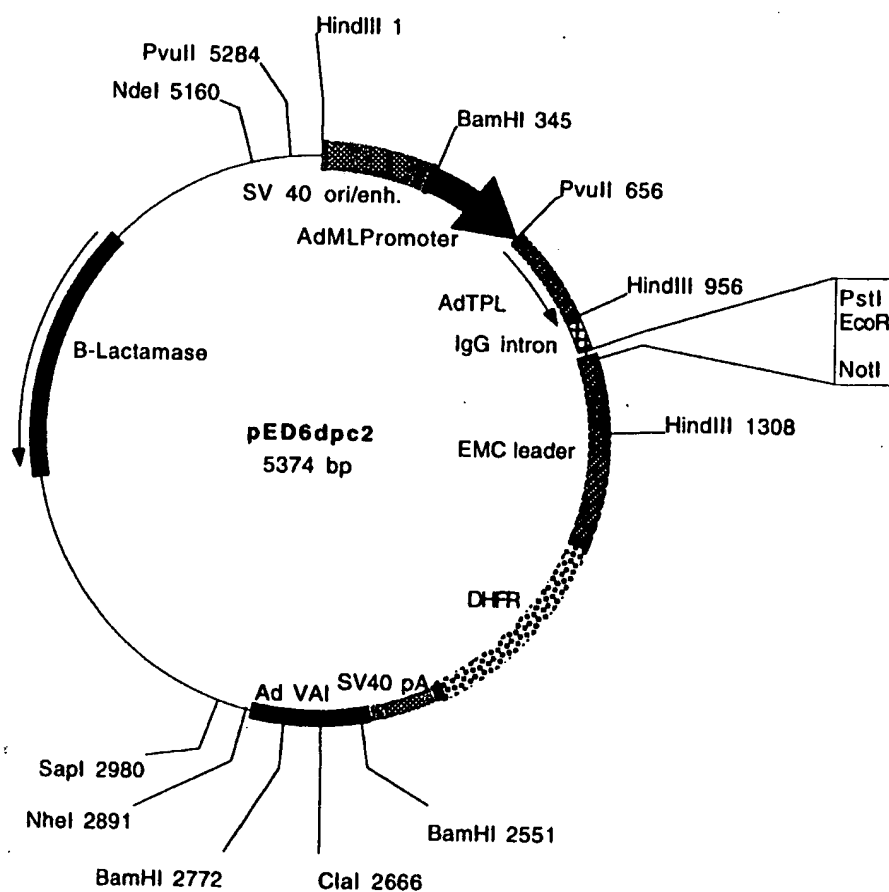
- (a) the amino acid sequence of SEQ ID NO:16;
- (b) the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 58;

(c) fragments of the amino acid sequence of SEQ ID NO:16 comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:16; and

(d) the amino acid sequence encoded by the cDNA insert of clone fr473\_2 deposited under accession number ATCC 98415; the protein being substantially free from other mammalian proteins.

32. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:15.

FIGURE 1A

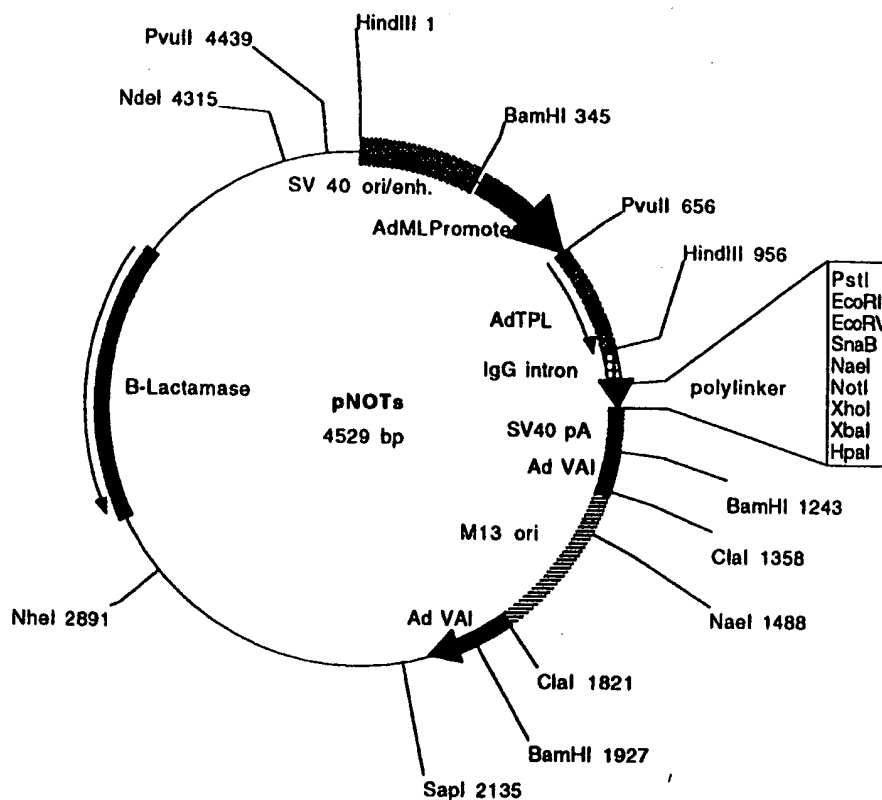


**Plasmid name:** pED6dpc2

**Plasmid size:** 5374 bp

**Comments/References:** pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 1B



**Plasmid name:** pNOTs

**Plasmid size:** 4529 bp

**Comments/References:** pNOTs is a derivative of pMT2 (Kaufman et al, 1989. Mol. Cell. Biol. 9:1741-1750). DHFR was deleted and a new polylinker was inserted between EcoRI and HpaI. M13 origin of replication was inserted in the ClaI site. SST cDNAs are cloned between EcoRI and NotI

## INTERNATIONAL SEARCH REPORT

International Application No

PC1/JS 98/08336

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/47 A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0 383 129 A (MOLECULAR DIAGNOSTICS INC.) 22 August 1990 see page 9, line 35-44 see page 9 - page 10; claims see figures 8,11,13 ---	1-11
A	WO 97 07198 A (GENETICS INSTITUTE INC.) 27 February 1997 ---	
A	US 5 536 637 A (JACOBS KENNETH) 16 July 1996 cited in the application -----	

☐ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents :

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

\*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

\*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

\*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

\*Z\* document member of the same patent family

Date of the actual completion of the international search

8 July 1998

Date of mailing of the international search report

08.10.98

Name and mailing address of the ISA

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Authorized officer

Macchia, G

# INTERNATIONAL SEARCH REPORT

I. International application No.

PCT/US 98/ 08336

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-11

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.



**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

**1. Claims: 1-11**

Polynucleotide comprising the nucleotide sequence of Seq.ID:1 and encoding a polypeptide of Seq.ID:2 or fragments. Polynucleotide fragments, variants, homologues, gene thereof. Host cell transformed with said polynucleotide. Protein comprising an amino acid sequence of Seq.ID:2 or fragments thereof. Process for producing said protein.

**2. Claims: 12-14**

Polynucleotide comprising the nucleotide sequence of Seq.ID:3 and encoding a polypeptide of Seq.ID:4 or fragments. Polynucleotide fragments, variants, homologues, gene thereof. Protein comprising an amino acid sequence of Seq.ID:4 or fragments thereof.

**3. Claims: 15-17**

As invention 2 but concerning Seq.ID:5 and 6.

**4. Claims: 18-20**

As invention 2 but concerning Seq.ID:7 and 8.

**5. Claims: 21-23**

As invention 2 but concerning Seq.ID:9 and 10.

**6. Claims: 24-26**

As invention 2 but concerning Seq.ID:11 and 12.

**7. Claims: 27-29**

As invention 2 but concerning Seq.ID:13 and 14.

**8. Claims: 30-32**

As invention 2 but concerning Seq.ID:15 and 16.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/JS 98/08336

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